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- (71) Applicant (*for all designated States except US*): **EPIGENOMICS AG [DE/DE]; Kastanienallee 24, 10435 Berlin (DE).**
- (72) Inventor; and
- (75) Inventor/Applicant (*for US only*): **BERLIN, Kurt [DE/DE]; Marienkäferweg 4, 14532 Stahnsdorf (DE).**
- (74) Agent: **SCHUBERT, Klemens; Neue Promenade 5, 10178 Berlin (DE).**
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(54) Title: **METHOD FOR ANALYSIS OF METHYLATED NUCLEIC ACIDS**

(57) **Abstract**: A method is disclosed providing analysis of the degree of methylation within nucleic acid samples, including the degree of methylation within CpG islands. After bisulfite treatment of a nucleic acid sample to convert cytosines to uracils, multiple species of paired oligonucleotide primers and optionally a methylation insensitive reference primer pair are used to amplify target sequences within the sample by methylation specific PCR. Amplification of multiple primer pairs is combined with the use of a real time PCR. Amplificates of primer pairs are detected and quantified by comparison, thus allowing for a detailed, more specific, and quantifiable analysis of the methylation status within a complex CpG methylation pattern of a nucleic acid sample. Primer pairs and a kit are also disclosed.